

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: HIRANO, TOSHIO
KAISHO, TSUNEYASU
- (ii) TITLE OF INVENTION: MEMBRANE PROTEIN POLYPEPTIDE HAVING
PRE-B CELL GROWTH-SUPPORTING ABILITY AND A GENE THEREOF
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
(B) STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
(C) CITY: ARLINGTON
(D) STATE: VA
(E) COUNTRY: USA
(F) ZIP: 22202
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/624,650
(B) FILING DATE: 22-MAY-1996
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/JP94/01732
(B) FILING DATE: 14-OCT-1994
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: JP 5-281622
(B) FILING DATE: 15-OCT-1993
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: OBLON, NORMAN F.
(B) REGISTRATION NUMBER: 24,618
(C) REFERENCE/DOCKET NUMBER: 7625-001-0 PCT
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 703-413-3000
(B) TELEFAX: 703-413-2220

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Ala Ser Thr Ser Tyr Asp Tyr Cys Arg Val Pro Met Glu Asp Gly
1 5 10 15
Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile Gly Ile Leu Val Leu Leu
20 25 30
Ile Ile Val Ile Leu Gly Val Pro Leu Ile Ile Phe Thr Ile Lys Ala
35 40 45
Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg
50 55 60
Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly
65 70 75 80
Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met
85 90 95
Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys
100 105 110
Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln
115 120 125
Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
130 135 140
Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
145 150 155 160
Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser
165 170 175
Ala Leu Leu Gln
180

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 996 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTGGAATTCA TGGCATCTAC TTCGTATGAC TATTGCAGAG TGCCCATGGA AGACGGGGAT	60
AAGCGCTGTA AGCTTCTGCT GGGGATAGGA ATTCTGGTGC TCCTGATCAT CGTGATTCTG	120
GGGGTGCCCT TGATTATCTT CACCATCAAG GCCAACAGCG AGGCCTGCCG GGACGGCCTT	180
CGGGCAGTGA TGGAGTGTCT CAATGTCACC CATCTCCTGC AACAAAGAGCT GACCGAGGCC	240
CAGAAGGGCT TTCAGGATGT GGAGGCCAG GCCGCCACCT GCAACCACAC TGTGATGGCC	300
CTAATGGCTT CCCTGGATGC AGAGAAGGCC CAAGGACAAA AGAAAGTGGG GGAGCTTGAG	360
GGAGAGATCA CTACATTAAA CCATAAGCTT CAGGACGCGT CTGCAGAGGT GGAGCGACTG	420
AGAAGAGAAA ACCAGGTCTT AAGCGTGAGA ATCGCGGACA AGAAGTACTA CCCCAGCTCC	480
CAGGACTCCA GCTCCGCTGC GGCGCCCCAG CTGCTGATTG TGCTGCTGGG CCTCAGCGCT	540
CTGCTGCAGT GAGATCCCAG GAAGCTGGCA CATCTTGGAA GGTCCGTCCT GCTCGGCTTT	600
TGGCTTGAAC ATTCCCTTGA TCTCATCAGT TCTGAGCGGG TCATGGGGCA ACACGGTTAG	660
CGGGGAGAGC ACGGGGTAGC CGGAGAAGGG CCTCTGGAGC AGGTCTGGAG GGGCCATGGG	720
GCAGTCCTGG GTGTGGGGAC ACAGTCGGGT TGACCCAGGG CTGTCTCCCT CCAGAGCCTC	780
CCTCCGGACA ATGAGTCCCC CCTCTTGTCT CCCACCCTGA GATTGGGCAT GGGGTGCGGT	840
GTGGGGGGCA TGTGCTGCCT GTTGTTATGG GTTTTTTTTG CGGGGGGGGT TGCTTTTTTC	900
TGGGGTCTTT GAGCTCCAAA AAATAAACAC TTCCTTTGAG GGAGAGCAAA AAAAAAAAAA	960
AAAAAAAAAA AAAAAAAAAA AAAGAATTCC ACCACA	996